# Double stochastic Poisson process can reproduce spiking statistics of cortical neurons

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## Abstract

*Cortical neurons of behaving animals generate irregular spike sequences. This suggests that a neuron receives highly fluctuated synaptic inputs. If the input fluctuation is large relatively to the mean, then spikes would be randomly discharged due to the rate determined by the mean and the fluctuation. When the incoming synaptic inputs are uncorrelated, such a random spiking mechanism generates a entirely random spike sequence at a constant rate (Poisson process), because the mean and the fluctuation are constant. Otherwise, temporally correlated inputs cause the spike rate to be variable, and this type of spike event process corresponds to a 'double stochastic Poisson process'.*

*In the present paper, we attempt to determine whether this simple spiking mechanism can statistically reproduce the spiking data recorded in monkey prefrontal cortices. Model parameters are estimated from the auto-correlogram of a spike sequence, and the consistency is examined based on the statistical coefficients of inter-spike intervals. It is found that a 'double stochastic Poisson process' can reproduce the interval statistics of the biological spiking data consistently with the auto-correlogram.*

## 1 Introduction

A cortical neuron under a constant current injection *in vitro* generates regular spike sequences with almost constant intervals [1]. On the other hand, a neuron *in vivo* generates irregular spike sequences including highly variable intervals [2][3]. This suggests that a neuron *in vivo* receives highly fluctuated synaptic inputs. With inhibition balanced to excitation in the incoming inputs, the fluctuation becomes large relatively to the mean, and spikes are randomly discharged [4]. The random spike sequence (Poisson process) exhibits high variability in its intervals. So this scenario is consistent with biological spiking variability. But many biological spike sequences differ from the Poisson process in statistical coefficients of inter-spike intervals[5].

Shinomoto, Sakai and Funahashi (1999) [5] attempted to determine whether the simple leaky integrate-and-fire mechanism can reproduce the spiking statistics. They examined statistical coefficients of inter-spike interval distribution and the correlation coefficient of consecutive intervals estimated from the spiking data recorded in monkey prefrontal cortices. It was found that the leaky integrate-and-fire mechanism can not statistically reproduce the spiking data under the assumption of uncorrelated synaptic inputs. They led the necessity of temporal correlation with time scale on the order of 100 msec in the incoming inputs to reproduce the spiking statistics [6][7]. These studies suggest that the fast fluctuation and long time scale correlation in the synaptic inputs are essential factors to reproduce the spiking statistics. But they have not yet solved the problem of whether the integration mechanism in a cell is essential or not.

In this paper, we examine the effect of temporal integration on the spiking statistics by considering a simple random spiking mechanism without any temporal integration in a neuron. When the mean of incoming inputs is too small to produce a spike by itself and the fast fluctuation is dominant in spiking, spikes are randomly emitted due to the rate determined by only the mean and the fluctuation at each moment. With temporally correlated inputs, the spike rate is variable. A neuron receives synaptic inputs from a large number of neurons, so its spike has little influ-

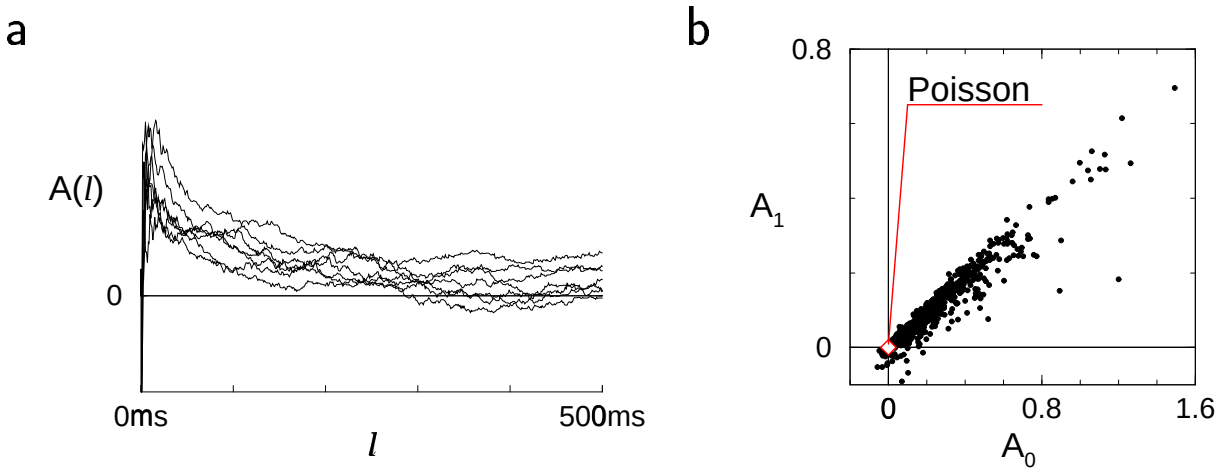


Figure 1: a: Examples of the normalized auto-correlogram $A(l)$ estimated from the biological spiking data. b: Each dot represents two cumulative coefficients of auto-correlation, $(A_0, A_1)$, estimated from a prepared set of biological spike sequences. The plot includes 666 dots respectively corresponding to 666 prepared data sets. The values $(A_0, A_1) = (0, 0)$ are given by the Poisson process (random sequence).

ence on the incoming inputs through possible recurrent connections. Therefore the spike rate is considered to be independent from its spike events. This type of spike event process is called as 'double stochastic Poisson process'. In this mechanism, the effect of input fluctuation is adopt as the random spiking, and the effect of input correlation is adopt as the slowly changing rate. We attempt to determine whether the simple 'double stochastic Poisson process' can statistically reproduce the biological spiking data.

## 2 Biological data and Statistics

In this paper, we analyze delay period activities of cortical neurons in a delay response task experiment. The detail of the experiment is shown in [5].

In the experiment, a monkey is required to preserve a visual cue information presented in advance during 3 second delay period. Iterating the experiment, the spiking data were obtained from total 233 neurons in the prefrontal cortices of three monkeys. We use only the middle 2 sec in the delay period of 3 sec in order to avoid the possible initial and final transient changes. The 2 sec spike sequences are classified according to the cues and the neurons, and 1864 sets (233 neurons $\times$ 8 cues) of spike sequences are obtained. In this paper, we do the statistical operations for one set of spike sequences. For reliable statistical analyses, we adopt only the sets including more than 100 spikes. The data sets containing more than 100 spikes are 666 of 1864.

We analyze the prepared data sets in two ways: auto-correlogram of a spike sequence, and statistical coefficients of an inter-spike interval sequence.

***Statistics of auto-correlation*** The spike auto-correlation function is defined as a function of time lag $l$, $\langle \lambda(t)\lambda(t+l)\rangle$, where $\lambda(t)$ is spike probability per unit time at time $t$, and the notation $\langle \cdots \rangle$ represents a temporal averaging operation: $\langle f(t)\rangle = \lim_{t\to\infty} \frac{1}{t}\int_0^t f(t)dt$. The 'auto-correlogram' is the estimate from finite data, which is defined as the frequency histogram of events that spikes are observed in both of the two time windows separated by lag $l$. If the spike sequence has no temporal correlation, then the auto-correlation is equal to the square of the mean spike rate, $\langle \lambda(t)\lambda(t+l)\rangle = \langle\lambda\rangle^2$. Here we define a normalized auto-correlation function: $A(l)$,

$$A(l) \equiv \frac{\langle \lambda(t)\lambda(t+l)\rangle}{\langle\lambda\rangle^2} - 1 \ .$$

The quantity of $A(l)$ has no dimension. The sign of $A(l)$ corresponds to the sign of correlation at lag $l$ in the sequence. Some examples of $A(l)$ estimated from the biological spiking data are shown in Figure 1a. Most of the spiking data exhibit positive correlations, whose shapes are similar to exponential functions.

In this paper, we use the normalized auto-correlogram $A(l)$ to estimate the model parameters, but the auto-correlogram itself largely depends on the width of histogram time bin. Accordingly, the estimation of $A(l)$ contains arbitrariness of the analyzer. So we define cumulative quantities of auto-correlation

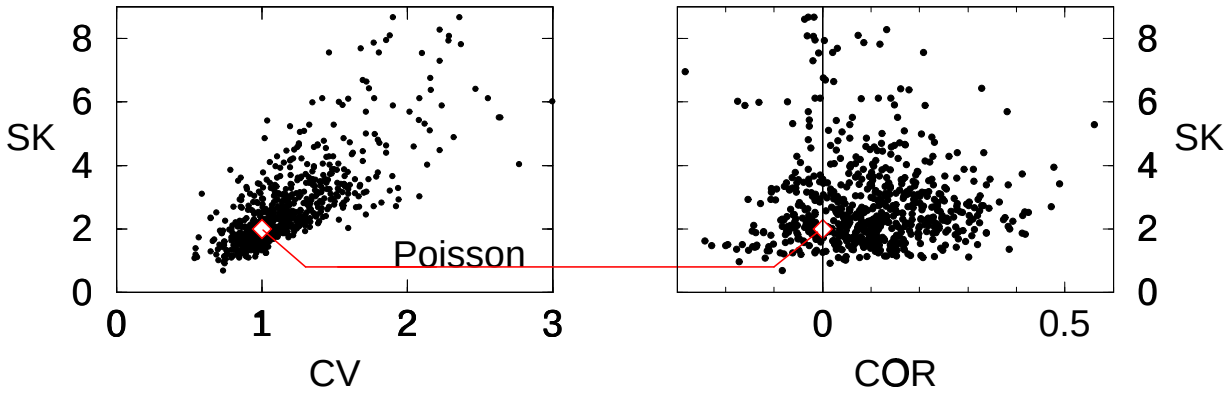


Figure 2: Each dot represents the statistical coefficients (CV, SK) values (in left plot) and (COR, SK) values (in right plot) estimated from a prepared set of biological spike sequences. Each plot includes 666 dots corresponding to 666 prepared data sets. The values (CV, SK, COR) = (1, 2, 0) are given by the Poisson process (random sequence).

with no need of time bin,

$$A_k \equiv \int_0^\infty l^k A(l) dl \ .$$

The correlation is not considered to last infinitely, so each of the cumulative coefficients $\{A_k\}$ has finite value. When a set of $N$ sequences with length $L$ is given, the cumulative coefficients $\{A_k\}$ are estimated without use of the explicit auto-correlogram or histogram bin as follows,

$$\begin{aligned} A_k &\approx \int_0^M l^k A(l) dl \\ &= \sum_{0<l_{ij}<M} \frac{l_{ij}^k}{\langle\lambda\rangle(\langle\lambda\rangle - 1/L)(L - l_{ij})} - M \ , \end{aligned}$$

where $l_{ij}$ represents a time lag from the $i$-th spike to the $j$-th spike, $l_{ij} = t_j - t_i$. The $M$ represents the integral range. Because the sequences have finite length $L$, the integral range is required to be also finite, $M \leq L$. The factor $\langle\lambda\rangle(\langle\lambda\rangle - 1/L)$ corresponds to the normalizing factor, which is revised from $\langle\lambda\rangle^2$ for the sake of unbiased estimation. The factor $(L - l_{ij})$ corresponds to the range of averaging time at lag $l_{ij}$. In the prepared data set, the sequence length $L$ of each trial is equal to 2 sec, and we settle the integral length $M$ on 1 sec ($L = 2, M = 1$). The number of trials, $N$, varies with each data set.

If all of the $\{A_k\}$ are equal to zero, then the sequence has no correlation, which corresponds to a random spike sequence (Poisson process). If each $A_k$ has positive value, then the ratio $A_{k+1}/A_k$ characterizes the sustaining time scale of positive correlation. In the case of exponential correlation, $A(l) \propto \exp(-l/s)$, the ratio $A_{k+1}/A_k$ is exactly equal to the correlation time scale, $s$.

The values of $(A_0, A_1)$ estimated from the 666 sets of biological spiking data are plotted in Figure 1b. Most data have positive $(A_0, A_1)$ values. It shows that the spiking data have positive temporal correlation. We use these two coefficients to estimate the model parameters.

***Statistics of inter-spike intervals*** We examine a spiking model through comparison with biological spiking data based on three statistical coefficients of inter-spike intervals: the coefficient of variation CV, the skewness coefficient SK, and the correlation coefficient of consecutive intervals COR, defined as,

$$\begin{aligned} \mathrm{CV} &\equiv \frac{\sqrt{\overline{(T - \overline{T})^2}}}{\overline{T}} \ , \\ \mathrm{SK} &\equiv \frac{\overline{(T - \overline{T})^3}}{\sqrt{\overline{(T - \overline{T})^2}}^{\,3}} \ , \\ \mathrm{COR} &\equiv \frac{\overline{(T_i - \overline{T})(T_{i+1} - \overline{T})}}{\overline{(T - \overline{T})^2}} \ , \end{aligned}$$

where $T$ represents an inter-spike interval, and $\{T_1, T_2, ..., T_i, ..., T_n\}$ is an interval sequence. The notation $\overline{\cdots}$ represents an averaging operation through

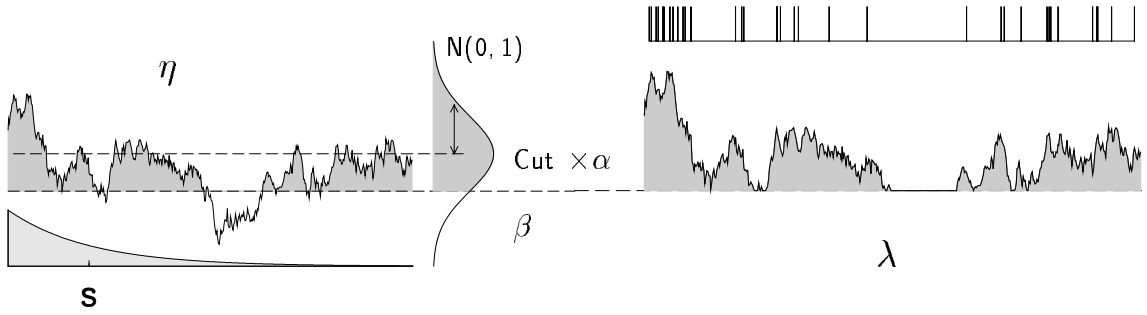


Figure 3: Schematic representation of a simple random spiking model belonging to a double stochastic Poisson process.

an interval sequence: $\overline{T} = \frac{1}{n} \sum_{i=1}^{n} T_i$. The coefficient of variation CV is a measure of variability of intervals, which shows a measure of spiking irregularity[2]. The skewness coefficient SK is a measure of the asymmetry of the interval distribution, which shows a measure of anomalous long intervals[10][5]. The correlation coefficient COR is a serial correlation coefficient at lag 1 in an interval sequence, which shows a measure of temporal correlation[11][6].

The coefficients (CV, SK, COR) values estimated from the spiking data are plotted in Figure 2. Any random sequence (Poisson process) gives the coefficient values, (CV, SK, COR)=(1, 2, 0). The biological (CV, SK, COR) values are largely distributed around those of Poisson process, (1, 2, 0). It has been found that the Poisson process can not statistically reproduce these (CV, SK, COR) values [6].

## 3 A double stochastic Poisson process

With inhibition balanced to excitation in incoming inputs, the mean could be small relatively to the fluctuation [4]. When the mean is too small to emit a spike by itself and a spike is emitted by the instantaneous fluctuation, the temporal integration in a neuron has little effect on the spike probability. In this case, spikes are randomly emitted due to the rate $\lambda(t)$ determined by the mean and fluctuation at each moment. Here we will call this spiking mechanism as 'random spiking mechanism'. We attempt to examine the effect of temporal integration by considering the random spiking mechanism without temporal integration.

In the random spiking mechanism, uncorrelated inputs lead to constant spike rate, $\lambda(t) = \lambda_0$, and the spike sequence corresponds to a Poisson process. Otherwise, temporally correlated inputs lead to variable spike rate. When spike rate $\lambda(t)$ is independent from its spike events, the spike event process is called as 'double stochastic Poisson process'. A neuron receives synaptic inputs from a large number of neurons, so its spike has little influence on the incoming inputs, even if the network has recurrent connections. Therefore the double stochastic Poisson process is naturally derived from the random spiking assumption.

The auto-correlation function of the spike rate $\lambda(t)$ is equal to the spike auto-correlation. The spike auto-correlograms of the spiking data are similar to exponential functions, so we assume that the auto-correlation function of $\lambda(t)$ is described by an exponential function,

$$\langle \lambda(t)\lambda(t+l) \rangle = (\langle \lambda^2 \rangle - \langle \lambda \rangle^2)\, e^{-l/s} + \langle \lambda \rangle^2 \ ,$$

where $s$ is correlation time scale.

The Ornstein-Uhlenbeck process $\eta$ has an exponential correlation function: $\langle \eta(t)\eta(t+l) \rangle \propto e^{-l/s}$. It is a well-known one variable stochastic process described as $s\dot{\eta} = -\eta + \xi$, where $\xi$ is white Gaussian noise. Here we assume the spike rate $\lambda(t)$ to be simply described with the Ornstein-Uhlenbeck process as,

$$\begin{aligned} s\,\dot{\eta} &= -\eta + \sqrt{2}\,\xi \ , \\ \lambda(\eta) &= \begin{cases} \alpha(\eta - \beta) & (\eta \geq \beta) \\ 0 & (\eta < \beta) \end{cases} \ . \end{aligned}$$

The process is represented schematically in Figure 3. We can regard $\eta$ as the mean or the fluctuation of incoming synaptic inputs, or some statistical quantity among the presynaptic neurons.

The Ornstein-Uhlenbeck process has a steady distribution of $N(0, 1)$ (normal distribution). Therefore the three model parameters $(s, \alpha, \beta)$ are easily estimated from the spike frequency $\langle \lambda \rangle$, and the cumulative coefficients of auto-correlation, $(A_0, A_1)$, by solving the coupling equations as follows,

$$\langle \lambda \rangle = \int_{\beta}^{\infty} \frac{\alpha(\eta - \beta)}{\sqrt{2\pi}}\, e^{-\eta^2/2} d\eta \ ,$$

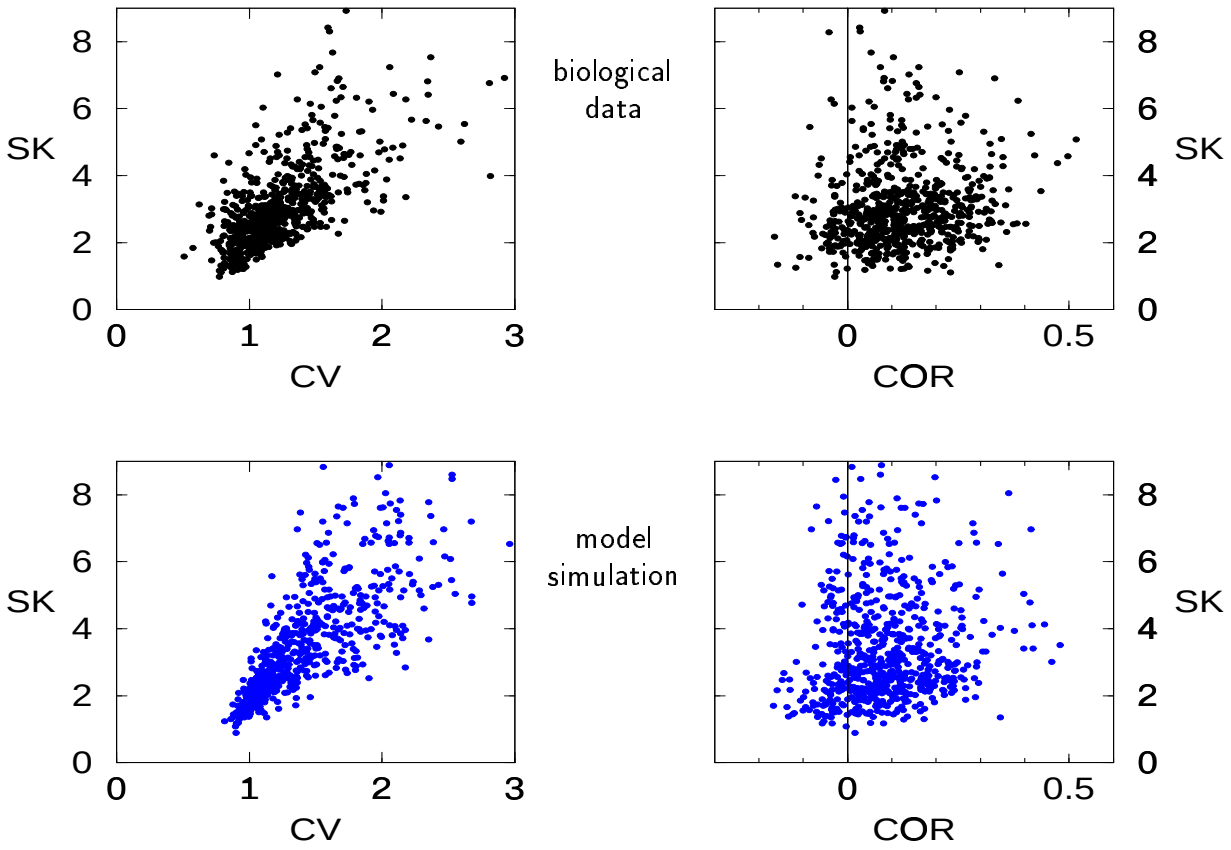


Figure 4: Comparison of the model simulation with the biological spiking data based on the statistical coefficients of inter-spike intervals, (CV, SK, COR).

$$\langle \lambda^2 \rangle = \int_\beta^\infty \frac{\alpha^2(\eta-\beta)^2}{\sqrt{2\pi}} e^{-\eta^2/2} d\eta \ ,$$

$$A_0 = \frac{\langle \lambda^2 \rangle - \langle \lambda \rangle^2}{\langle \lambda \rangle^2} \int_0^M e^{-l/s} dl \ ,$$

$$A_1 = \frac{\langle \lambda^2 \rangle - \langle \lambda \rangle^2}{\langle \lambda \rangle^2} \int_0^M l \ e^{-l/s} dl \ .$$

In the next section, we simulate this simple model at the parameters estimated from the auto-correlation statistics $(\langle \lambda \rangle, A_0, A_1)$, and attempt to determine whether the model can reproduce the interval statistics (CV, SK, COR)

## 4 Model simulation

The model parameters $(s, \alpha, \beta)$ are estimated from the auto-correlation statistics $(\langle \lambda \rangle, A_0, A_1)$, which are estimated from each set of the biological spike sequences. The interval statistics (CV, SK, COR) are also estimated from the same data set. We numerically simulate the model under the same condition as the experiment: the same trial length and the same number of trials. We calculate the coefficients (CV, SK, COR) by the same method from the obtained artificial data set. We compare the coefficients (CV, SK, COR) between the simulation and the biological data set. Each simulation does well reproduce the interval statistics (CV, SK, COR). We plot the biological and artificial (CV, SK, COR) values about whole 666 data sets in Figure4. The projected shapes of the coefficients distribution are very similar to each other. We iterate the simulation 1000 times per a data set, and estimate each significance value of the coefficients (CV, SK, COR). The minimum significance value is 1.1% ($P > 0.011$). It is enough larger than $1/666 = 0.0015$.

Even the highly simplified random spiking model has sufficient ability to reproduce the interval statistics consistently with the auto-correlation statistics. It

implies that the temporal integration mechanism has little effect on the spiking statistics, at least for the biological spiking data we prepared.

## 5 Discussion

In the previous studies, it was found that highly fluctuated and slowly correlated inputs are needed for the leaky integrate-and-fire mechanism to reproduce the spiking statistics of neurons in prefrontal cortex [5][6]. In this paper, we attempted to examine the effect of temporal integration on the spiking statistics, by considering a simple random spiking mechanism without any temporal integration in a neuron. We found that even a highly simplified random spiking mechanism has sufficient ability to reproduce the statistics of inter-spike intervals consistently with the statistics of auto-correlation as long as the incoming inputs have long time scale correlation. It implies that the temporal integration in a cell has little effect on the spiking statistics. It is possible that a cortical neuron performs the statistical operation through the presynaptic neurons at each instance rather than the temporal operation on the history of synaptic inputs, while a neuron has the ability of performing complex temporal operations[14].

The random spiking mechanism shares a common point with the 'coincidence detector' advanced by Abeles[12][13]. The temporal integration is neglected in both. But the random spiking mechanism bases on highly fluctuated inputs, while the 'coincidence detector' bases on a specific temporal pattern of coincidently incoming inputs. This difference leads to the problem of what is the carrier of information in such a noisy spike sequence. We hope to solve the problem in the future.

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